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RAW SEQUENCE LISTING

DATE: 09/20/2002

PATENT APPLICATION: US/09/833,017B

TIME: 13:41:12

Input Set : A:\EP.txt

Output Set: N:\CRF3\09202002\I833017B.raw

3 <110> APPLICANT: CVITKOVITCH, Dennis
 5 <120> TITLE OF INVENTION: SIGNAL PEPTIDES NUCLEIC ACID MOLECULES AND METHODS FOR
 TREATMENT OF
 6 CARIES
 8 <130> FILE REFERENCE: 1889/00401
 10 <140> CURRENT APPLICATION NUMBER: 09/833,017B
 11 <141> CURRENT FILING DATE: 2001-04-10
 13 <160> NUMBER OF SEQ ID NOS: 30
 15 <170> SOFTWARE: PatentIn version 3.0
 17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 141
 19 <212> TYPE: DNA
 20 <213> ORGANISM: Streptococcus mutans
 22 <220> FEATURE:
 23 <221> NAME/KEY: CDS
 24 <222> LOCATION: (1)..(141)
 26 <400> SEQUENCE: 1
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 28 Met Lys Lys Thr Leu Ser Leu Lys Asn Asp Phe Lys Glu Ile Lys Thr
 29 5 10 15
 31 gat gaa tta gag att atc att ggc gga agc gga agc cta tca aca ttt 96
 32 Asp Glu Leu Glu Ile Ile Gly Gly Ser Gly Ser Leu Ser Thr Phe
 33 20 25 30
 35 ttc cgg ctg ttt aac aga agt ttt aca caa gct ttg gga aaa taa 141
 36 Phe Arg Leu Phe Asn Arg Ser Phe Thr Gln Ala Leu Gly Lys
 37 35 40 45
 40 <210> SEQ ID NO: 2
 41 <211> LENGTH: 46
 42 <212> TYPE: PRT
 43 <213> ORGANISM: Streptococcus mutans
 45 <400> SEQUENCE: 2
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 48 1 5 10 15
 51 Asp Glu Leu Glu Ile Ile Gly Gly Ser Gly Ser Leu Ser Thr Phe
 52 20 25 30
 55 Phe Arg Leu Phe Asn Arg Ser Phe Thr Gln Ala Leu Gly Lys
 56 35 40 45
 59 <210> SEQ ID NO: 3
 60 <211> LENGTH: 63
 61 <212> TYPE: DNA
 62 <213> ORGANISM: Streptococcus mutans
 64 <220> FEATURE:
 65 <221> NAME/KEY: CDS
 66 <222> LOCATION: (1)..(63)

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68 <400> SEQUENCE: 3
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 70 Ser Gly Ser Leu Ser Thr Phe Phe Arg Leu Phe Asn Arg Ser Phe Thr
 71 1 5 10 15
 73 caa gct ttg gga aaa . 63
 74 Gln Ala Leu Gly Lys
 75 20
 78 <210> SEQ ID NO: 4
 79 <211> LENGTH: 21
 80 <212> TYPE: PRT
 81 <213> ORGANISM: Streptococcus mutans
 83 <400> SEQUENCE: 4
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 86 1 5 10 15
 89 Gln Ala Leu Gly Lys
 90 20
 93 <210> SEQ ID NO: 5
 94 <211> LENGTH: 1326
 95 <212> TYPE: DNA
 96 <213> ORGANISM: Streptococcus mutans
 98 <220> FEATURE:
 99 <221> NAME/KEY: CDS
 100 <222> LOCATION: (1)..(1326)
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 104 Met Asn Glu Ala Leu Met Ile Leu Ser Asn Gly Leu Leu Thr Tyr Leu
 105 1 5 10 15
 107 acc gtt cta ttt ctc ttg ttt cta ttt tct aag gta agt aat gtc act 96
 108 Thr Val Leu Phe Leu Leu Phe Ser Lys Val Ser Asn Val Thr
 109 20 25 30
 111 tta tcg aaa aag gaa tta act ctt ttt tcg ata agc aat ttt ctg ata 144
 112 Leu Ser Lys Lys Glu Leu Thr Leu Phe Ser Ile Ser Asn Phe Leu Ile
 113 35 40 45
 115 atg att gct gtt acg atg gtg aac gta aac ctg ttt tat cct gca gag 192
 116 Met Ile Ala Val Thr Met Val Asn Val Asn Leu Phe Tyr Pro Ala Glu
 117 50 55 60
 119 cct ctt tat ttt ata gct tta tca att tat ctt aat aga cag aat agt 240
 120 Pro Leu Tyr Phe Ile Ala Leu Ser Ile Tyr Leu Asn Arg Gln Asn Ser
 121 65 70 75 80
 123 ctt tct cta aat ata ttt tat ggt ctg ctg cct gtt gcc agt tct gac 288
 124 Leu Ser Leu Asn Ile Phe Tyr Gly Leu Leu Pro Val Ala Ser Ser Asp
 125 85 90 95
 127 ttg ttt agg cgg gca atc ata ttc ttt atc ttg gat gga act caa gga 336
 128 Leu Phe Arg Arg Ala Ile Ile Phe Phe Ile Leu Asp Gly Thr Gln Gly
 129 100 105 110
 131 att gta atg ggc agt agc att ata acc acc tat atg atc gag ttt gca 384
 132 Ile Val Met Gly Ser Ser Ile Ile Thr Thr Tyr Met Ile Glu Phe Ala
 133 115 120 125
 135 gga ata gcg cta agt tac ctc ttt ctc agt gtg ttc aat gtt gat att 432

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136	Gly	Ile	Ala	Leu	Ser	Tyr	Leu	Phe	Leu	Ser	Val	Phe	Asn	Val	Asp	Ile	
137	130						135					140					
139	ggt	cga	ctt	aaa	gat	agt	ttg	acc	aag	atg	aag	gtc	aaa	aaa	cgc	ttg	480
140	Gly	Arg	Leu	Lys	Asp	Ser	Leu	Thr	Lys	Met	Lys	Val	Lys	Lys	Arg	Leu	
141	145						150				155				160		
143	att	cca	atg	aat	att	act	atg	ctt	cta	tac	tac	ctt	tta	ata	cag	gta	528
144	Ile	Pro	Met	Asn	Ile	Thr	Met	Leu	Leu	Tyr	Tyr	Leu	Leu	Ile	Gln	Val	
145							165				170			175			
147	ttg	tat	gtt	ata	gag	agt	tat	aat	gtg	ata	ccg	act	tta	aaa	ttt	cgt	576
148	Leu	Tyr	Val	Ile	Glu	Ser	Tyr	Asn	Val	Ile	Pro	Thr	Leu	Lys	Phe	Arg	
149							180				185			190			
151	aaa	ttt	gtc	gtt	att	gtc	tat	ctt	att	tta	ttt	ttg	att	ctg	atc	tca	624
152	Lys	Phe	Val	Val	Ile	Val	Tyr	Leu	Ile	Leu	Phe	Leu	Ile	Leu	Ile	Ser	
153							195			200			205				
155	ttt	tta	agc	caa	tat	acc	aaa	caa	aag	gtt	caa	aat	gag	ata	atg	gca	672
156	Phe	Leu	Ser	Gln	Tyr	Thr	Lys	Gln	Lys	Val	Gln	Asn	Glu	Ile	Met	Ala	
157							210			215			220				
159	caa	aag	gaa	gct	cag	att	cga	aat	atc	acc	cag	tat	agt	cag	caa	ata	720
160	Gln	Lys	Glu	Ala	Gln	Ile	Arg	Asn	Ile	Thr	Gln	Tyr	Ser	Gln	Gln	Ile	
161							225			230			235			240	
163	gaa	tct	ttt	tac	aag	gat	att	cga	agt	ttc	cgc	cat	gat	tat	ctg	aat	768
164	Glu	Ser	Leu	Tyr	Lys	Asp	Ile	Arg	Ser	Phe	Arg	His	Asp	Tyr	Leu	Asn	
165							245			250			255				
167	att	tta	act	agc	ctc	aga	tta	ggc	att	gaa	aat	aaa	gat	tta	gct	agt	816
168	Ile	Leu	Thr	Ser	Leu	Arg	Leu	Gly	Ile	Glu	Asn	Lys	Asp	Leu	Ala	Ser	
169							260			265			270				
171	att	gaa	aag	att	tac	cat	caa	atc	tta	gaa	aaa	aca	gga	cat	caa	ttg	864
172	Ile	Glu	Lys	Ile	Tyr	His	Gln	Ile	Leu	Glu	Lys	Thr	Gly	His	Gln	Leu	
173							275			280			285				
175	cag	gat	acc	cgt	tat	aat	atc	ggc	cat	cta	gct	aat	att	caa	aac	gat	912
176	Gln	Asp	Thr	Arg	Tyr	Asn	Ile	Gly	His	Ile	Leu	Ala	Asn	Ile	Gln	Asn	Asp
177							290			295			300				
179	gct	gtc	aag	ggt	atc	ttg	tca	gca	aaa	atc	tta	gaa	gct	cag	aat	aaa	960
180	Ala	Val	Lys	Gly	Ile	Leu	Ser	Ala	Lys	Ile	Leu	Glu	Ala	Gln	Asn	Lys	
181							305			310			315			320	
183	aag	att	gct	gtc	aat	gta	gaa	gtc	tca	agt	aaa	ata	caa	ctg	cct	gag	1008
184	Lys	Ile	Ala	Val	Asn	Val	Glu	Val	Ser	Ser	Lys	Ile	Gln	Leu	Pro	Glu	
185							325			330			335				
187	atg	gag	ttg	ctt	gat	ttc	att	acc	ata	ctt	tct	atc	ttg	tgt	gat	aat	1056
188	Met	Glu	Leu	Leu	Asp	Phe	Ile	Thr	Ile	Leu	Ser	Ile	Leu	Cys	Asp	Asn	
189							340			345			350				
191	gcc	att	gag	gct	gtc	ttc	gaa	tca	tta	aat	cct	gaa	att	cag	tta	gcc	1104
192	Ala	Ile	Glu	Ala	Ala	Phe	Glu	Ser	Leu	Asn	Pro	Glu	Ile	Gln	Leu	Ala	
193							355			360			365				
195	ttt	ttt	aag	aaa	aat	ggc	agt	ata	gtc	ttt	atc	att	cag	aat	tcc	acc	1152
196	Phe	Phe	Lys	Lys	Asn	Gly	Ser	Ile	Val	Phe	Ile	Ile	Gln	Asn	Ser	Thr	
197							370			375			380				
199	aaa	gaa	aaa	caa	ata	gat	gtg	agt	aaa	att	ttt	aaa	gaa	aac	tat	tcc	1200
200	Lys	Glu	Lys	Gln	Ile	Asp	Val	Ser	Lys	Ile	Phe	Lys	Glu	Asn	Tyr	Ser	

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201	385	390	395	400	
203	act aaa ggc tcc aat cgc ggt att ggt tta gca aag gtg aat cat att				1248
204	Thr Lys Gly Ser Asn Arg Gly Ile Gly Leu Ala Lys Val Asn His Ile				
205	405	410	415		
207	c当地t gaa cat tat ccc aaa acc agt tta caa aca agc aat cat cat cat				1296
208	Leu Glu His Tyr Pro Lys Thr Ser Leu Gln Thr Ser Asn His His His				
209	420	425	430		
211	tta ttc aag caa ctc cta ata ata aaa tag				1326
212	Leu Phe Lys Gln Leu Leu Ile Ile Lys				
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216	<210> SEQ ID NO: 6				
217	<211> LENGTH: 441				
218	<212> TYPE: PRT				
219	<213> ORGANISM: Streptococcus mutans				
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223	Met Asn Glu Ala Leu Met Ile Leu Ser Asn Gly Leu Leu Thr Tyr Leu				
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227	Thr Val Leu Phe Leu Leu Phe Leu Ser Lys Val Ser Asn Val Thr				
228	20	25	30		
231	Leu Ser Lys Lys Glu Leu Thr Leu Phe Ser Ile Ser Asn Phe Leu Ile				
232	35	40	45		
235	Met Ile Ala Val Thr Met Val Asn Val Asn Leu Phe Tyr Pro Ala Glu				
236	50	55	60		
239	Pro Leu Tyr Phe Ile Ala Leu Ser Ile Tyr Leu Asn Arg Gln Asn Ser				
240	65	70	75	80	
243	Leu Ser Leu Asn Ile Phe Tyr Gly Leu Leu Pro Val Ala Ser Ser Asp				
244	85	90	95		
247	Leu Phe Arg Arg Ala Ile Ile Phe Phe Ile Leu Asp Gly Thr Gln Gly				
248	100	105	110		
251	Ile Val Met Gly Ser Ser Ile Ile Thr Thr Tyr Met Ile Glu Phe Ala				
252	115	120	125		
255	Gly Ile Ala Leu Ser Tyr Leu Phe Leu Ser Val Phe Asn Val Asp Ile				
256	130	135	140		
259	Gly Arg Leu Lys Asp Ser Leu Thr Lys Met Lys Val Lys Lys Arg Leu				
260	145	150	155	160	
263	Ile Pro Met Asn Ile Thr Met Leu Leu Tyr Tyr Leu Leu Ile Gln Val				
264	165	170	175		
267	Leu Tyr Val Ile Glu Ser Tyr Asn Val Ile Pro Thr Leu Lys Phe Arg				
268	180	185	190		
271	Lys Phe Val Val Ile Val Tyr Leu Ile Leu Phe Leu Ile Leu Ile Ser				
272	195	200	205		
275	Phe Leu Ser Gln Tyr Thr Lys Gln Lys Val Gln Asn Glu Ile Met Ala				
276	210	215	220		
279	Gln Lys Glu Ala Gln Ile Arg Asn Ile Thr Gln Tyr Ser Gln Gln Ile				
280	225	230	235	240	
283	Glu Ser Leu Tyr Lys Asp Ile Arg Ser Phe Arg His Asp Tyr Leu Asn				
284	245	250	255		
287	Ile Leu Thr Ser Leu Arg Leu Gly Ile Glu Asn Lys Asp Leu Ala Ser				
288	260	265	270		

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291	Ile	Glu	Lys	Ile	Tyr	His	Gln	Ile	Leu	Glu	Lys	Thr	Gly	His	Gln	Leu
292	275				280				285							
295	Gln	Asp	Thr	Arg	Tyr	Asn	Ile	Gly	His	Leu	Ala	Asn	Ile	Gln	Asn	Asp
296	290				295				300							
299	Ala	Val	Lys	Gly	Ile	Leu	Ser	Ala	Lys	Ile	Leu	Glu	Ala	Gln	Asn	Lys
300	305				310				315							320
303	Lys	Ile	Ala	Val	Asn	Val	Glu	Val	Ser	Ser	Lys	Ile	Gln	Leu	Pro	Glu
304					325				330							335
307	Met	Glu	Leu	Leu	Asp	Phe	Ile	Thr	Ile	Leu	Ser	Ile	Leu	Cys	Asp	Asn
308					340				345							350
311	Ala	Ile	Glu	Ala	Ala	Phe	Glu	Ser	Leu	Asn	Pro	Glu	Ile	Gln	Leu	Ala
312					355				360							365
315	Phe	Phe	Lys	Lys	Asn	Gly	Ser	Ile	Val	Phe	Ile	Ile	Gln	Asn	Ser	Thr
316					370				375							380
319	Lys	Glu	Lys	Gln	Ile	Asp	Val	Ser	Lys	Ile	Phe	Lys	Glu	Asn	Tyr	Ser
320					385				390							400
323	Thr	Lys	Gly	Ser	Asn	Arg	Gly	Ile	Gly	Leu	Ala	Lys	Val	Asn	His	Ile
324					405				410							415
327	Leu	Glu	His	Tyr	Pro	Lys	Thr	Ser	Leu	Gln	Thr	Ser	Asn	His	His	His
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331	Leu	Phe	Lys	Gln	Leu	Leu	Ile	Ile	Lys							
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336	<211>	LENGTH:	750													
337	<212>	TYPE:	DNA													
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347	1				5				10							15
349	ctt	gaa	acc	acc	att	gca	gct	atc	atc	aaa	gaa	aaa	aat	tgg	tct	tat
350	Leu	Glu	Thr	Thr	Ile	Ala	Ala	Ile	Met	Lys	Glu	Lys	Asn	Trp	Ser	Tyr
351					20				25							30
353	aaa	gaa	ttt	act	att	ttt	gga	aaa	cca	caa	caa	ctt	att	gac	gct	atc
354	Lys	Glu	Leu	Thr	Ile	Phe	Gly	Lys	Pro	Gln	Gln	Leu	Ile	Asp	Ala	Ile
355					35				40							45
357	cct	gaa	aag	ggc	aat	cac	cag	att	tcc	ttt	ttg	gat	att	gaa	atc	aaa
358	Pro	Glu	Lys	Gly	Asn	His	Gln	Ile	Phe	Phe	Leu	Asp	Ile	Glu	Ile	Lys
359					50				55							60
361	aaa	gag	gaa	aag	aaa	gga	ctg	gaa	gtt	gcc	aat	cag	att	aga	cag	cat
362	Lys	Glu	Glu	Lys	Gly	Leu	Glu	Val	Ala	Asn	Gln	Ile	Arg	Gln	His	
363					65				70							80
365	aat	cct	agt	gca	gtt	att	gtc	ttt	gtc	acg	aca	cat	tct	gag	ttt	atg
366	Asn	Pro	Ser	Ala	Val	Ile	Val	Phe	Val	Thr	Thr	His	Ser	Glu	Phe	Met
367					85				90							95
369	ccc	ctc	act	ttt	cag	tat	cag	gtt	tct	gct	ttg	gat	ttt	att	gat	aaa
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VERIFICATION SUMMARY

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L:683 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:20
L:696 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:21
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